

Replacement Sheet

FIGURE 7

Predicted twin-arginine (RR-)signal peptides of *B. subtilis*¹

| Protein | N | h | RR-Motif | SEQ ID NO: | H | h | C |
|--------------------|---|------|---------------|------------------|----|-----|-----|
| AlbB | 1 | 0.1 | RRILL | 30 | 27 | 2.0 | AIA |
| AmyX TM | 9 | -0.8 | RRSFE | 31 | 15 | 1.1 | - |
| AppB TM | 8 | 0.5 | RRTLm | 32 | 19 | 2.3 | - |
| LipA | 7 | -1.1 | RRIIA | 33 | 19 | 1.2 | AKA |
| OppB TM | 8 | -0.6 | RRLVY | 34 | 24 | 2.0 | - |
| PbpX | 2 | -2.2 | RRRKL | 35 | 14 | 2.9 | WNA |
| PhoD | 3 | -1.3 | RRKFI | 36 | 17 | 0.9 | VGA |
| QcrA TM | 1 | -1.1 | RRQFL | 37 | 19 | 1.3 | - |
| TlpA TM | 1 | -0.8 | RRLII | 38 | 21 | 2.4 | - |
| WapA ^w | 1 | -3.0 | RRNFK | 39 | 18 | 2.3 | VLA |
| WprA | 8 | -1.7 | RRKFS | 40 | 20 | 1.9 | AAA |
| YceA TM | 1 | -0.4 | RR AFL | 41 | 21 | 2.2 | - |
| YesM TM | 1 | -1.5 | RRMKI | 42 | 20 | 2.4 | QYA |
| YesW | 1 | -1.3 | RRSCL | 43 | 19 | 2.0 | VKA |
| YfkN TM | 1 | -1.2 | RRTHV | 44 | 17 | 1.7 | IHA |
| YkpC | 8 | -1.0 | RRVAI | 45 | 17 | 2.3 | SLA |
| YkuE | 1 | -1.3 | RRQFL | 46 | 17 | 1.0 | GYA |
| YmaC | 7 | 0.0 | RRFLL | 47 | 15 | 2.4 | YSL |
| YubF TM | 9 | -2.7 | RRNTV | 48 | 23 | 2.0 | - |
| YuiC | 8 | 0.2 | RRLLM | 49 | 20 | 1.9 | IEA |
| YvhJ TM | 2 | -1.7 | RRKIL | 50 | 18 | 2.5 | - |
| YwbN | 1 | -1.8 | RRDIL | 51 | 23 | 1.4 | QTA |

¹The listed signal peptides contain, in addition to the twin-arginines, at least one other residue of the consensus sequence (R-R-X-Φ-Φ; printed in bold). The number of residues in the N- and H-domains of each signal peptide, and the average hydrophobicity (h) of each of these domains, as determined by the algorithms of Kyte and Doolittle (Kyte, J., and R. F. Doolittle [1982] A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* 157:105-32), are indicated. Furthermore, the RR-motifs in the N-domain, and SPaseI recognition sites in the C-domain (*ie.* positions -3 to -1 relative to the predicted SPaseI cleavage site) are shown. Proteins lacking a (putative) SPaseI cleavage site, some of which contain additional transmembrane domains, are indicated with TM. One protein containing cell wall binding repeats is indicated with ^w.